

us-10-007-047-1.rni

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 02:15:21 ; Search time 689 seconds  
(without alignments)  
10767.603 Million cell updates/secTitle: US-10-007-047-1  
Perfect score: 4534  
Sequence: 1 ccaagcttggtacccccggg.....gcatgcnntagagggcccta 4534Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summariesDatabase : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3855	85.0	6628	4	US-09-949-016-4586	Sequence 4586, Ap
2	3754.8	82.8	4796	3	US-09-085-199B-3	Sequence 3, Appli
3	1664.4	36.7	2301	3	US-09-085-199B-8	Sequence 8, Appli
4	1155.2	25.5	1164	3	US-09-085-199B-1	Sequence 1, Appli
5	1118.4	24.7	3715	3	US-09-085-199B-44	Sequence 44, Appl
6	1116.8	24.6	68702	4	US-09-949-016-16328	Sequence 16328, A
7	970	21.4	3979	3	US-09-085-199B-10	Sequence 10, Appl
8	715.4	15.8	3876	4	US-09-849-602-4	Sequence 4, Appli
9	483.2	10.7	3251	3	US-09-085-199B-6	Sequence 6, Appli
10	187	4.1	436	3	US-09-085-199B-28	Sequence 28, Appl
c 11	187	4.1	601	4	US-09-949-016-163605	Sequence 163605,
12	175.4	3.9	279	3	US-09-085-199B-43	Sequence 43, Appl
13	149	3.3	485	3	US-09-085-199B-32	Sequence 32, Appl
14	147.2	3.2	193	3	US-09-085-199B-17	Sequence 17, Appl
15	144.6	3.2	578	3	US-09-085-199B-25	Sequence 25, Appl
16	144	3.2	565	3	US-09-085-199B-23	Sequence 23, Appl
17	138.8	3.1	498	3	US-09-085-199B-36	Sequence 36, Appl

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	18	136.6	3.0	468	3	US-09-085-199B-33	Sequence 33, Appl
	19	126.6	2.8	418	3	US-09-085-199B-42	Sequence 42, Appl
c	20	126.2	2.8	601	4	US-09-949-016-163634	Sequence 163634,
	21	125	2.8	359	3	US-09-085-199B-30	Sequence 30, Appl
c	22	116	2.6	510	4	US-09-270-767-928	Sequence 928, App
c	23	116	2.6	510	4	US-09-270-767-16210	Sequence 16210, A
	24	114	2.5	427	3	US-09-085-199B-37	Sequence 37, Appl
c	25	113.4	2.5	601	4	US-09-949-016-163645	Sequence 163645,
c	26	113.4	2.5	601	4	US-09-949-016-163646	Sequence 163646,
c	27	113.4	2.5	601	4	US-09-949-016-163647	Sequence 163647,
	28	111.2	2.5	421	3	US-09-085-199B-35	Sequence 35, Appl
c	29	111.2	2.5	601	4	US-09-949-016-163613	Sequence 163613,
	30	110.8	2.4	351	3	US-09-085-199B-41	Sequence 41, Appl
	31	105.6	2.3	437	3	US-09-085-199B-40	Sequence 40, Appl
	32	104.2	2.3	209	3	US-09-085-199B-31	Sequence 31, Appl
c	33	103	2.3	601	4	US-09-949-016-163567	Sequence 163567,
	34	102	2.2	390	3	US-09-085-199B-26	Sequence 26, Appl
c	35	102	2.2	601	4	US-09-949-016-163602	Sequence 163602,
	36	98.6	2.2	502	3	US-09-085-199B-39	Sequence 39, Appl
c	37	98.6	2.2	601	4	US-09-949-016-163624	Sequence 163624,
c	38	98.6	2.2	601	4	US-09-949-016-163626	Sequence 163626,
c	39	98.6	2.2	601	4	US-09-949-016-163627	Sequence 163627,
c	40	98.2	2.2	601	4	US-09-949-016-163625	Sequence 163625,
	41	92.8	2.0	393	3	US-09-085-199B-34	Sequence 34, Appl
	42	90.8	2.0	8078	3	US-09-702-251-3	Sequence 3, Appli
	43	89.4	2.0	469	3	US-09-085-199B-29	Sequence 29, Appl
	44	80.4	1.8	327	3	US-09-085-199B-20	Sequence 20, Appl
	45	79.8	1.8	3489	2	US-08-728-323A-1	Sequence 1, Appli

# RESULT 8

US-09-849-602-4

; Sequence 4, Application US/09849602

; Patent No. 6794501

; GENERAL INFORMATION:

; APPLICANT: Scanlan, Matthew J.

; APPLICANT: Old, Lloyd J.

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Chen, Yao-Tseng

; TITLE OF INVENTION: Colon Cancer Antigen Panel

; FILE REFERENCE: L0461/7105(JRV)

; CURRENT APPLICATION NUMBER: US/09/849,602

; CURRENT FILING DATE: 2001-05-04

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 3876

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-849-602-4

Query Match 15.8%; Score 715.4; DB 4; Length 3876;  
 Best Local Similarity 56.9%; Pred. No. 1e-190;  
 Matches 1458; Conservative 0; Mismatches 1006; Indels 99; Gaps 4;

QY	619	ATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGTATTCAACTCCCTGGAC	678
Db	1	ATGTTTGATTACATGGATTGTGAGCTGAAGCTTTCTGAATCAGTTTTCCGACAGCTCAAC	60
QY	679	ATGTCCCCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCTCGCCCCGCTGATCCAG	738
Db	61	ACGGCCATCGCCGTATCCCAGATGTCCTCAGGCCAGTGCCGCCTGGCCCCCCTCATCCAG	120

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Qy	739	GTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCTTCTCTTCAAACCTCCAC	798
Db	121	GTCATCCAGGACTGCAGCCACCTCTACCACTACACGGTCAAGCTCCTGTTCAAGCTACAC	180
Qy	799	TCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGACCGCTTCATGGAGCAGTTTACA	858
Db	181	TCTTGTCTCCCTGCGGACACCCTGCAAGGCCACAGGGACCGGTTCCACGAGCAGTTTCAC	240
Qy	859	AAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTTCAAGCGGCTCATTGAG	918
Db	241	AGCCTCAGGAACTTCTTCCGAGAGCCTCCGACATGCTGTACTTCAAGCGGCTCATCCAG	300
Qy	919	ATCCCCCAGCTGCCTGAGAACCCACCAACTTCCTGCGAGCCTCAGCCCTGTCAGAACAT	978
Db	301	ATCCCCCGGCTGCCCGAGGGACCCCTAACTTCCTGCGGGCCTCAGCCCTGGCTGAGCAC	360
Qy	979	ATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCCGACAGCGAGCCAGTCCTA	1038
Db	361	ATCAAGCCGGTGGTGGTGATCCCCGAGGAGGCCCC-----GGAAGATGAG	405
Qy	1039	GAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTTATTTGACAACAAGTTT	1098
Db	406	GAGCCGGAGAATCTCATTGAGATCAGCACAGGGCCCCCGCGGGGAGCCAGTGGTGGTG	465
Qy	1099	GATGACATCTTTGGCAGTTCATTGAGCAGTGATCCCTTCAATTTCAACAGTCAAAATGGT	1158
Db	466	GCTGACCTCTTCGATCAGACGTTTGG-----ACCCCCAATGGG	504
Qy	1159	GTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAGAGAGATCAGTGGATTG	1218
Db	505	TCTGTGAAGGACGACAGGGACCTCCAGATTGAGAGCTTGAAGAGAGAGGTGGAAATGCTC	564
Qy	1219	AAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGTTGTGCTGCAGCTGAAGGGC	1278
Db	565	CGCTCTGAACTGGAGAAGATCAAGCTGGAGGCCAGCGGTACATCGCGCAGCTGAAGAGC	624
Qy	1279	CACGTGAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCTGCGGCAGCAGGCGGCC	1338
Db	625	CAGGTGAATGCACTGGAGGGTGAGCTGGAGGAGCAGCGGAAGCAGAAGGAGGCCCTG	684
Qy	1339	GACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAGGCAGCGGGAGGACACC	1398
Db	685	GTGGATAATGAGCAGCTCCGCCACGAGCTGGCCAGCTGAGGGCTGCCAGCTGGAGGGC	744
Qy	1399	GAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCAAGCCAATGAACAGCGA	1458
Db	745	GAGCGGAGCCAGGGCCTGCGTGAGGAGGCTGAGAGGAAGGCCAGTGCCACGGAGGCGCGC	804
Qy	1459	TATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCACGCTGACCTGCTGCGG	1518
Db	805	TACAACAAGCTGAAGGAAAAGCACAGTGAGCTCGTCCATGTGCACGCGGAGCTGCTCAGA	864
Qy	1519	AAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGCCCAGGTAGATTTGGAA	1578
Db	865	AAGAACGCGGACACAGCCAAGCAGCTGACGGTGACGCAGCAAAGCCAGGAGGAGGTGGCG	924
Qy	1579	CGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGACCAGGGCCAGCGGAAG	1638
Db	925	CGGGTGAAGGAGCAGCTGGCCTTCCAGGTGGAGCAGGTGAAGCGGGAGTCGGAGTTGAAG	984
Qy	1639	ACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACTTGCCACAAGCCAACGG	1698

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Db 985 CTAGAGGAGAAGAGCGACCAGCTGGAGAAGCTCAAGAGGGAGCTGGAGGCCAAGGCCGGA 1044  
 Qy 1699 GAGCTTCAGGTTCTGCAAGGCAGCCTGGAACTTCTGCCCAGTCAGAAGCAAAGTGGGCA 1758  
 Db 1045 GAGCTGGCCCGCGCGCAGGAGGCCCTGAGCCACACAGAGCAGAGCAAGTCGGAGCTGAGC 1104  
 Qy 1759 GCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAGTGGCGCAGCTCATAGG 1818  
 Db 1105 TCACGGCTGGACACGCTGAGTGCGGAGAAGGATGCTCTGAGTGGAGCTGTGCGGCAGCGG 1164  
 Qy 1819 GAGGAGGAATTATCTGCTCTTCGAAAGAACTGCAGGACACTCAGCTCAAAGTGGCCAGC 1878  
 Db 1165 GAGGCAGACCTGCTGGCGGCGCAGAGCCTGGTGCGCGAGACAGAGGCGGCGCTGAGCCGG 1224  
 Qy 1879 ACAGAG-----GAATCTATGTGCCAGCTTGCCAAAGACCAA 1914  
 Db 1225 GAGCAGCAGCGCAGCTCCCAGGAGCAGGGCGAGTTGACAGGCGCGCTGGCAGAGAGGGAG 1284  
 Qy 1915 CGAAAAATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAG----- 1956  
 Db 1285 TCTCAGGAGCAGGGGCTGCGGCAGAGGCTGCTGGACGAGCAGTTCGCAGTGTGCGGGGC 1344  
 Qy 1957 -----GTGATACAAGACGCCCTGAACCAGCTTGAAGAACCTCCT 1995  
 Db 1345 GCTGCTGCCGAGGCCGCGGGCATCCTGCAGGATGCCGTGAGCAAGCTGGACGACCCCTG 1404  
 Qy 1996 CTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCACATCCATTTCAGC 2055  
 Db 1405 CACCTGCGCTGTACCAGCTCCCAGACTACCTGGTGAGCAGGGCCAGGAGGCCTTGAT 1464  
 Qy 2056 TGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCAGAAAGACATCAGT 2115  
 Db 1465 GCCGTGAGCACCCTGGAGGAGGGCCACGCCAGTACCTGACCTCCTTGGCAGACGCCTCC 1524  
 Qy 2116 GGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGCCATTGCTCATGGT 2175  
 Db 1525 GCCCTGGTGGCAGCTCTGACCCGCTTCTCCACCTGGCTGCGGATACCATCATCAATGGC 1584  
 Qy 2176 GCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGACCGAGGCCTGTAAG 2235  
 Db 1585 GGTGCCACCTCGCACCTGGCTCCCACCGACCCTGCCGACCGCCTCATAGACACCTGCAGG 1644  
 Qy 2236 CAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGAGGGAAAGCCTTGAG 2295  
 Db 1645 GAGTGCGGGGCCGGGCTCTGGAGCTCATGGGGCAGCTGCAGGACCAGCAGGCTCTGCGG 1704  
 Qy 2296 AATGCCGACAGCACAGCCATGAGGAAGTGCCTGAGCAAGATCAAGGCCATCGGCGAGGAG 2355  
 Db 1705 CACATGCAGGCCAGCCTGGTGCGGACACCCCTGCAGGGCATCCTTCAGCTGGGCCAGGAA 1764  
 Qy 2356 CTCCTGCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCTGGTGGACAAGGAG 2415  
 Db 1765 CTGAAACCCAAGAGCCTAGATGTGCGGCAGGAGGAGCTGGGGGCCGTGGTGCACAAGGAG 1824  
 Qy 2416 ATGGCGGCCCACTTCAGCTGCTATTGAACTGCCACGGCCAGAATAGAGGAGATGCTCAGC 2475  
 Db 1825 ATGGCGGCCACATCCGCAGCCATTGAAGATGCTGTGCGGAGGATTGAGGACATGATGAAC 1884  
 Qy 2476 AAATCCCAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAGGATCCTTGTTGC 2535  
 Db 1885 CAGGCACGCCACGCCAGCTCGGGGGTGAAGCTGGAGGTGAACGAGAGGATCCTCAACTCC 1944  
 Qy 2536 TGTACCAGCCTCATGCAAGCTATTAGGTGCTCATCGTGGCCTCTAAGGACCTCCAGAGA 2595

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Db	1945	TGCACAGACCTGATGAAGGCTATCCGGCTCCTGGTGACGACATCCACTAGCCTGCAGAAG	2004
Qy	2596	GAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCCTAAAGAGTTTTATGCCAAGAACTCT	2655
Db	2005	GAGATCGTGGAGAGCGGCAGGGGGGCAGCCACGCAGCAGGAATTTTACGCCAAGAACTCG	2064
Qy	2656	CGATGGACAGAAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGGAGCCACTGTCATG	2715
Db	2065	CGCTGGACCGAAGGCCTCATCTCGGCCTCCAAGGCTGTGGGCTGGGGAGCCACACAGCTG	2124
Qy	2716	GTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGAGCTAATGGTGTGT	2775
Db	2125	GTGGAGGCAGCTGACAAGGTGGTGCTTACACGGGCAAGTATGAGGAGCTCATCGTCTGC	2184
Qy	2776	TCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAAGGTGAAAGCTGAT	2835
Db	2185	TCCCACGAGATCGCAGCCAGCACGGCCCAGCTGGTGGCGGCCCTCCAAGGTGAAGGCCAAC	2244
Qy	2836	AAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGAGTGAACCAGGCCACT	2895
Db	2245	AAGCACAGCCCCCACCTGAGCCGCCTGCAGGAATGTTCTCGCACAGTCAATGAGAGGGCT	2304
Qy	2896	GCCGGCGTTGTGGCCTCAACCATTTCGGGCAAATCACAGATCGAAGAGACAGACAACATG	2955
Db	2305	GCCAATGTGGTGGCCTCCACCAAGTCAGGCCAGGAGCAGATTGAGGACAGAGACACCATG	2364
Qy	2956	GACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGATTCTCAGGTTAGG	3015
Db	2365	GATTTCTCCGGCCTGTCCCTCATCAAGCTGAAGAAGCAGGAGATGGAGACGCAGGTGCGT	2424
Qy	3016	GTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAAGTGGGAGAGCTTCGGAAA	3075
Db	2425	GTCCTGGAGCTGGAGAAGACGCTGGAGGCTGAACGCATGCGGCTGGGGGAGTTGCGGAAG	2484
Qy	3076	AAGCACTACGAGCTTGCTGGTGTGCTGAGGGCTGGGAAGAAG	3118
Db	2485	CAACACTACGTGCTGGCTGGGGCATCAGGCAGCCCTGGAGAGG	2527